STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
   ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 10| 820,067

Source: TWO

Date Processed by STIC: 1-31-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/24/05

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: 10/820,067

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics / Wrapped Aminos   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .); this will prevent "wrapping."

2 ___ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering   The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length   Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6 ___ Patentin 2.0 "bug"   A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ___. Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES)   Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

8 ___ Skipped Sequences (NEW RULES)   Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.821 of Sequence Rules, use of <220> <221> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ___ Invalid <221> Response   Per 1.823 of Sequence Rules, the only valid <211> responses are Unknown, Artificial Sequence or scientific name (Genus/species). <220> <221> section is required when <211> response is Unknown or is Artificial Sequence

11 ___ Use of <220>   Sequence(s) ___ missing the <220> feature and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <211> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol 63, No 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ Patentin 2.0 "bug"   Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 01/31/2005
PATENT APPLICATION: US/10/820,067   TIME: 11:27:02

Input Set : D:\SEQLIST 8449-406 (as filed).TXT
Output Set: N:\CRF4\01312005\J820067.raw

```
 4 <110> APPLICANT: Fletchner, J.
 5         Prince-Cohane, K.
 6         Mehta, S.
 7         Slusarewicz, P.
 8         Andjelic, S.
 9         Barber, B.
11 <120> TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED
12         VACCINES AND IMMUNOTHERAPIES
15 <130> FILE REFERENCE: 8449-406-999
17 <140> CURRENT APPLICATION NUMBER: 10/820,067
18 <141> CURRENT FILING DATE: 2004-04-08
20 <150> PRIOR APPLICATION NUMBER: 60/462,469
21 <151> PRIOR FILING DATE: 2003-04-11
23 <150> PRIOR APPLICATION NUMBER: 60/463,746
24 <151> PRIOR FILING DATE: 2003-04-18
26 <150> PRIOR APPLICATION NUMBER: 60/503,417
27 <151> PRIOR FILING DATE: 2003-09-16
29 <160> NUMBER OF SEQ ID NOS: 926
31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 4
35 <212> TYPE: PRT
36 <213> ORGANISM: Malaria
38 <400> SEQUENCE: 1
39 Asn Ala Asn Pro
40  1
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 9
45 <212> TYPE: PRT
46 <213> ORGANISM: Unknown
48 <220> FEATURE:
49 <223> OTHER INFORMATION: HLA-A2 peptide binding motif
W--> 51 <221> NAME/KEY: VARIANT
52 <222> LOCATION: 2
53 <223> OTHER INFORMATION: Xaa = Leu or Met
W--> 55 <221> VARIANT
56 <222> LOCATION: 6
57 <223> OTHER INFORMATION: Xaa = Val or Ile or Leu or Thr
W--> 59 <221> VARIANT
60 <222> LOCATION: 9
61 <223> OTHER INFORMATION: Xaa = Val or Leu
W--> 63 <221> VARIANT
64 <222> LOCATION: 1,3 , 4, 5, 7, 8
```

(p5.6)

**Does Not Comply
Corrected Diskette Needed**
(p5.2,3)

RAW SEQUENCE LISTING   DATE: 01/31/2005
PATENT APPLICATION: US/10/820,067   TIME: 11:27:02

Input Set : D:\SEQLIST 8449-406 (as filed).TXT
Output Set: N:\CRF4\01312005\J820067.raw

```
        65 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 67 <400> 2
W--> 68 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        69  1                 5
        72 <210> SEQ ID NO: 3
        73 <211> LENGTH: 9
        74 <212> TYPE: PRT
        75 <213> ORGANISM: Unknown
        77 <220> FEATURE:
        78 <223> OTHER INFORMATION: HLA-A2 peptide binding motif
W--> 80 <221> NAME/KEY: VARIANT
        81 <222> LOCATION: 2
        82 <223> OTHER INFORMATION: Xaa = Leu or Met
W-->. 84 <221> VARIANT
        85 <222> LOCATION: 1, 3, 4, 5, 6, 7, 8
        86 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 88 <400> 3
W--> 89 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val
        90  1                 5
        93 <210> SEQ ID NO: 4
        94 <211> LENGTH: 8
        95 <212> TYPE: PRT
        96 <213> ORGANISM: Unknown
        98 <220> FEATURE:
        99 <223> OTHER INFORMATION: HLA-A2 peptide binding motif
W--> 101 <221> NAME/KEY: VARIANT
       102 <222> LOCATION: 2
       103 <223> OTHER INFORMATION: Xaa = Val or Gln
W--> 105 <221> VARIANT
       106 <222> LOCATION: 1, 3, 4, 5, 6, 7, 8
       107 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 109 <400> 4
W--> 110 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu
       111  1                 5
       114 <210> SEQ ID NO: 5
       115 <211> LENGTH: 5
       116 <212> TYPE: PRT
       117 <213> ORGANISM: Unknown
       119 <220> FEATURE:
       120 <223> OTHER INFORMATION: HLA-DR peptide binding motif
       122 <400> SEQUENCE: 5
       123 Gln Lys Arg Ala Ala
       124  1                 5
       127 <210> SEQ ID NO: 6
       128 <211> LENGTH: 5
       129 <212> TYPE: PRT
       130 <213> ORGANISM: Unknown
       132 <220> FEATURE:
       133 <223> OTHER INFORMATION: HLA-DR peptide binding motif
```

(8) - Leu is at this location.

```
                    RAW SEQUENCE LISTING              DATE: 01/31/2005
                    PATENT APPLICATION:  US/10/820,067   TIME: 11:27:02

                    Input Set : D:\SEQLIST 8449-406 (as filed).TXT
                    Output Set: N:\CRF4\01312005\J820067.raw

        135 <400> SEQUENCE: 6
        136 Arg Arg Arg Ala Ala
        137  1               5
        140 <210> SEQ ID NO: 7
        141 <211> LENGTH: 7
        142 <212> TYPE: PRT
        143 <213> ORGANISM: Unknown
        145 <220> FEATURE:
        146 <223> OTHER INFORMATION: motif in heptamiric region recognized by heat
        147       shock protein
W--> 149 <221> NAME/KEY: VARIANT
        150 <222> LOCATION: 2
        151 <223> OTHER INFORMATION: Xaa = Trp or any amino acid
W--> 153 <221> VARIANT
        154 <222> LOCATION: 1, 3, 5, 7
        155 <223> OTHER INFORMATION: Xaa = hydrophobic amino acid residues
W--> 157 <221> VARIANT
        158 <222> LOCATION: 4, 6
        159 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 161 <400> 7
W--> 162 Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        163  1               5
        166 <210> SEQ ID NO: 8
        167 <211> LENGTH: 7
        168 <212> TYPE: PRT
        169 <213> ORGANISM: Unknown
        171 <220> FEATURE:
        172 <223> OTHER INFORMATION: motif in heptamiric region recognized by heat
        173       shock protein
W--> 175 <221> NAME/KEY: VARIANT
        176 <222> LOCATION: 2
        177 <223> OTHER INFORMATION: Xaa = Trp or any amino acid
W--> 179 <221> VARIANT
        180 <222> LOCATION: 1, 3, 5, 7,
        181 <223> OTHER INFORMATION: Xaa = hydrophobic amino acid residue, particularly
        182       tryptophan, leucine or phenylalanine
W--> 184 <221> VARIANT
        185 <222> LOCATION: 4, 6
        186 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 188 <400> 8
W--> 189 Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        190  1               5
        193 <210> SEQ ID NO: 9
        194 <211> LENGTH: 4
        195 <212> TYPE: PRT
        196 <213> ORGANISM: Artificial Sequence
        198 <220> FEATURE:
        199 <221> NAME/KEY: VARIANT
        200 <222> LOCATION: 1
```

See item # 11 on error summary sheet.

pls explain source of genetic material.

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

```
      201 <223> OTHER INFORMATION: Xaa = Ala/Ser/Val/Lys/Glu/Gly/Leu
      203 <220> FEATURE:
      204 <223> OTHER INFORMATION: In the order of preference, with Ala the most preferred
      206 <220> FEATURE:
      207 <221> NAME/KEY: VARIANT
      208 <222> LOCATION: 2
      209 <223> OTHER INFORMATION: Xaa = Lys/Val/Glu
      211 <220> FEATURE:
      212 <223> OTHER INFORMATION: In the order of preference, with Lys the most preferred
      214 <220> FEATURE:
      215 <221> NAME/KEY: VARIANT
      216 <222> LOCATION: 3
      217 <223> OTHER INFORMATION: Xaa = Val/Ser/Phe/Thr/Lys/Ala/Glu
      219 <220> FEATURE:
      220 <223> OTHER INFORMATION: In the order of preference, with Val the most preferred
      222 <400> SEQUENCE: 9
W--> 223 Xaa Xaa Xaa Leu
      224  1
      227 <210> SEQ ID NO: 10
      228 <211> LENGTH: 10
      229 <212> TYPE: PRT
      230 <213> ORGANISM: Adeno Virus
      232 <400> SEQUENCE: 10
      233 Ser Gly Pro Ser Asn Thr Pro Pro Glu Ile
      234  1               5                 10
      237 <210> SEQ ID NO: 11
      238 <211> LENGTH: 11
      239 <212> TYPE: PRT
      240 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
      242 <400> SEQUENCE: 11
      243 Ser Gly Val Glu Asn Pro Gly Gly Tyr Cys Leu
      244  1               5                 10
      247 <210> SEQ ID NO: 12
      248 <211> LENGTH: 10
      249 <212> TYPE: PRT
      250 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
      252 <400> SEQUENCE: 12
      253 Lys Ala Val Tyr Asn Phe Ala Thr Cys Gly
      254  1               5                 10
      257 <210> SEQ ID NO: 13
      258 <211> LENGTH: 9
      259 <212> TYPE: PRT
      260 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
      262 <400> SEQUENCE: 13
      263 Arg Pro Gln Ala Ser Gly Val Tyr Met
      264  1               5
      267 <210> SEQ ID NO: 14
      268 <211> LENGTH: 9
      269 <212> TYPE: PRT
```

F

```
270 <213> ORGANISM: Lymphocytic Choriomeningitis Virus (LCMV)
272 <400> SEQUENCE: 14
273 Phe Gln Pro Gln Asn Gly Gln Phe Ile
274  1                 5
277 <210> SEQ ID NO: 15
278 <211> LENGTH: 9
279 <212> TYPE: PRT
280 <213> ORGANISM: Influenza Virus
282 <400> SEQUENCE: 15
283 Ile Glu Gly Gly Trp Thr Gly Met Ile
284  1                 5
287 <210> SEQ ID NO: 16
288 <211> LENGTH: 10
289 <212> TYPE: PRT
290 <213> ORGANISM: Influenza Virus
292 <400> SEQUENCE: 16
293 Thr Tyr Val Ser Val Ser Thr Ser Thr Leu
294  1                 5                 10
297 <210> SEQ ID NO: 17
298 <211> LENGTH: 8
299 <212> TYPE: PRT
300 <213> ORGANISM: Influenza Virus
302 <400> SEQUENCE: 17
303 Phe Glu Ala Asn Gly Asn Leu Ile
304  1                 5
307 <210> SEQ ID NO: 18
308 <211> LENGTH: 9
309 <212> TYPE: PRT
310 <213> ORGANISM: Influenza Virus
312 <400> SEQUENCE: 18
313 Ile Tyr Ser Thr Val Ala Ser Ser Leu
314  1                 5
317 <210> SEQ ID NO: 19
318 <211> LENGTH: 9
319 <212> TYPE: PRT
320 <213> ORGANISM: Influenza Virus
322 <400> SEQUENCE: 19
323 Thr Tyr Gln Arg Thr Arg Ala Leu Val
324  1                 5
327 <210> SEQ ID NO: 20
328 <211> LENGTH: 9
329 <212> TYPE: PRT
330 <213> ORGANISM: Influenza Virus
332 <400> SEQUENCE: 20
333 Cys Thr Glu Leu Lys Leu Ser Asp Tyr
334  1                 5
337 <210> SEQ ID NO: 21
338 <211> LENGTH: 8
339 <212> TYPE: PRT
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/31/2005
PATENT APPLICATION: US/10/820,067   TIME: 11:27:03

Input Set : D:\SEQLIST 8449-406 (as filed).TXT
Output Set: N:\CRF4\01312005\J820067.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1,2,3,4,5,6,7,8,9
Seq#:3; Xaa Pos. 1,2,3,4,5,6,7,8
Seq#:4; Xaa Pos. 1,2,3,4,5,6,7
Seq#:7; Xaa Pos. 1,2,3,4,5,6,7
Seq#:8; Xaa Pos. 1,2,3,4,5,6,7
Seq#:9; Xaa Pos. 1,2,3
Seq#:401; Xaa Pos. 7
Seq#:402; Xaa Pos. 3
Seq#:407; Xaa Pos. 2,6
Seq#:454; Xaa Pos. 5
Seq#:564; Xaa Pos. 7
Seq#:565; Xaa Pos. 3
Seq#:570; Xaa Pos. 2,6
Seq#:617; Xaa Pos. 5
Seq#:805; Xaa Pos. 7
Seq#:806; Xaa Pos. 3
Seq#:811; Xaa Pos. 2,6
Seq#:858; Xaa Pos. 5

```
L:51 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:55 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:63 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:67 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:80 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:84 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:88 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:101 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:105 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:109 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:149 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:153 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:157 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:161 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:175 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:179 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:188 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:501 M:283 W: Missing Blank Line separator, <400> field identifier
L:4951 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4955 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:401
L:4956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:401 after pos.:0
L:4968 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:4972 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:402
L:4973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:402 after pos.:0
L:5037 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5041 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:407
L:5042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:407 after pos.:0
L:5652 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5656 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:454
L:5657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:454 after pos.:0
L:7086 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:7090 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:564
L:7091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:564 after pos.:0
L:7103 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:7107 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:565
L:7108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:565 after pos.:0
L:7172 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:7176 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:570
L:7177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:570 after pos.:0
L:7787 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/820,067

DATE: 01/31/2005
TIME: 11:27:03

Input Set : D:\SEQLIST 8449-406 (as filed).TXT
Output Set: N:\CRF4\01312005\J820067.raw

```
L:7791 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:617
L:7792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:617 after pos.:0
L:10404 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:10408 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:805
L:10409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:805 after pos.:0
L:10422 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:10426 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:806
L:10427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:806 after pos.:0
L:10496 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:10500 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:811
L:10501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:811 after pos.:0
L:11158 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:11162 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:858
L:11163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:858 after pos.:0
```